

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
2 May 2002 (02.05.2002)

PCT

(10) International Publication Number
WO 02/34280 A2

- (51) International Patent Classification⁷: **A61K 38/00**
- (21) International Application Number: PCT/GB01/04739
- (22) International Filing Date: 25 October 2001 (25.10.2001)
- (25) Filing Language: English
- (26) Publication Language: English
- (30) Priority Data:
0026114.9 25 October 2000 (25.10.2000) GB
- (71) Applicant (*for all designated States except US*):
SMITHKLINE BEECHAM P.L.C. [GB/GB]; New Horizons Court, Brentford, Middlesex TW8 9EP (GB).
- (72) Inventors; and
- (75) Inventors/Applicants (*for US only*): **DAVIS, John, Beresford** [GB/GB]; GlaxoSmithKline, New Frontiers Science Park South, Third Avenue, Harlow, Essex CM19 5AW (GB). **GUNTHORPE, Martin, James** [GB/GB]; GlaxoSmithKline, New Frontiers Science Park South, Third Avenue, Harlow, Essex CM19 5AW (GB). **EGERTON, Julie** [GB/GB]; GlaxoSmithKline, New Frontiers Science Park South, Third Avenue, Harlow, Essex CM19 5AW (GB). **SMART, Darren** [GB/GB]; GlaxoSmithKline, New Frontiers Science Park South, Third Avenue, Harlow, Essex CM19 5AW (GB).
- (74) Agent: **GIDDINGS, Peter, John**; SmithKline Beecham, Corporate Intellectual Property (CN9.25.1), 980 Great West Road, Brentford, Middlesex TW8 9GS (GB).
- (81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.
- (84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).
- Published:**
— *without international search report and to be republished upon receipt of that report*
- For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.*

(54) Title: NEW USE

(57) Abstract: The use of VR4 polypeptides and polynucleotides in the design of protocols for the treatment of diseases of cartilage, such as hyaline-, fibro- and elastic-cartilage, or diseases of tissues where such cartilage is found including diseases or disorders affecting the larynx, auditory canal, intervertebral discs, ligaments, tendons and joint capsules, bone development including osteoporosis, diseases involving joint destruction and also pain linked to rheumatoid arthritis and osteoarthritis.



WO 02/34280 A2

New Use

Field of the Invention

This invention relates to new uses for polynucleotides and polypeptides encoded
5 by them, to their use in therapy and in identifying compounds which may be agonists,
antagonists and/or inhibitors which are potentially useful in therapy.

Summary of the Invention

In one aspect, the invention relates to new uses of the vanilloid 4 receptor
10 (hereinafter VR4) polypeptide. Such uses include the identification and development of
compounds useful in the treatment of diseases of cartilage such as hyaline-, fibro- and
elastic-cartilage, or diseases of the tissues where these are found. Examples of such
diseases include, but are not limited to, diseases or disorders affecting the larynx,
auditory canal, intervertebral discs, ligaments, tendons, joint capsules or bone
15 development including osteoporosis. In particular the invention concerns diseases
involving joint destruction and also pain linked to rheumatoid arthritis and osteoarthritis.
These disease indications are referred to herein as "the diseases". In a further aspect, the
invention relates to methods for treating conditions associated with VR4 imbalance or
mutation with the identified compounds. In a still further aspect, the invention relates to
20 diagnostic assays for detecting diseases or disorders associated with inappropriate VR4
activity or levels.

Description of the Invention

A cDNA encoding human VR4 has recently been described (patent application
25 no.EP202352.1 SmithKline Beecham; Strotmann, R. et al (2000) Nature Cell Biology 2:
695-702). VR4 has a similar predicted structure to vanilloid receptor-1 (VR1), possessing
an N-terminal domain containing ankyrin repeats, six transmembrane domains and a
predicted pore loop between the fifth and sixth transmembrane domains. Various cDNAs
have been published which may represent splice variants of the human VR4 gene, for
30 example Delany, N.S., et al (2000) Eur.J.Neurosci. 12: suppl. 11, 134.10 p306 who also
shows expression of VR4 in pancreas, prostate, placenta and trachea. In addition

species homologues comprising regions of homology to human VR4 are known, for example Suzuki, M., et al (1999) J.Biol.Chem. 275: 2756-2762.

The present invention is based on the surprising finding that VR4 is expressed at significantly higher levels in articular cartilage than in a wide range of other tissues tested. In addition isolated chondrocytes are shown to have an unusually high level of VR4 mRNA expression. The invention concerns the use of VR4 polypeptides and the polynucleotides encoding the polypeptides in the treatment of diseases involving cartilage. The polypeptides may be used directly in such treatment or may be used in screens to identify compounds useful in such treatment.

Thus in a first aspect, the present invention relates to the use of a compound selected from:

- (a) a VR4 polypeptide;
- (b) a compound which modulates the activity of a VR4 polypeptide;
- (c) a polynucleotide encoding a VR4 polypeptide; or

(d) an antisense polynucleotide to a polynucleotide encoding a VR4 polypeptide, for the manufacture of a medicament for treating diseases of cartilage and/or bone, or for the treatment of pain associated therewith.

Such diseases of cartilage include those involving hyaline-, fibro- and elastic-cartilage, or diseases of tissues where such cartilage is found including diseases or disorders affecting the larynx, auditory canal, intervertebral discs, ligaments, tendons and joint capsules. Diseases of bone include those of bone development including osteoporosis.

In a preferred embodiment the disease is one involving joint destruction, preferably rheumatoid arthritis or osteoarthritis.

In a further preferred embodiment the disease concerns pain associated with a disease involving joint destruction, preferably rheumatoid arthritis and osteoarthritis.

Compounds which modulate the activity of a VR4 polypeptide include compounds that activate the VR4 polypeptide and also compounds which inhibit the activity of a VR4 polypeptide.

VR4 polypeptides for use in the invention, either directly in the manufacture of a medicament or indirectly, for example when used in a screen to identify modulators of VR4 activity, include isolated polypeptides comprising an amino acid sequence which has at

least 95% identity, preferably at least 97-99% identity, to that of SEQ ID NO:2. Such polypeptides include those comprising the amino acid of SEQ ID NO:2.

Further VR4 polypeptides include isolated polypeptides in which the amino acid sequence has at least 95% identity, preferably at least 97-99% identity, to the amino acid sequence of SEQ ID NO:2. Such polypeptides include the polypeptides of SEQ ID NO:2.

Still further VR4 polypeptides include isolated polypeptides encoded by a polynucleotide comprising the sequence contained in SEQ ID NO:1.

The VR4 polypeptides may be in the form of the "mature" protein or may be a part of a larger protein such as a precursor or a fusion protein. It is often advantageous to include an additional amino acid sequence which contains secretory or leader sequences, pro-sequences, sequences which aid in purification such as multiple histidine residues, or an additional sequence for stability during recombinant production.

The VR4 polypeptides can be prepared in any suitable manner. Such polypeptides include isolated naturally occurring polypeptides, recombinantly produced polypeptides, synthetically produced polypeptides, or polypeptides produced by a combination of these methods. Means for preparing such polypeptides are well understood in the art.

For preparing VR4 polypeptides by recombinant means, a polynucleotide encoding a VR4 polypeptide can be used (hereinafter a "VR4 polynucleotide").

VR4 polynucleotides may be obtained, using standard cloning and screening techniques (Sambrook *et al.*, Molecular Cloning: A Laboratory Manual, 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y.(1989) and European patent application no. EP202352.1 (SmithKline Beecham), from a cDNA library derived from mRNA in cells of human osteoarthritic cartilage, heart, kidney or human brain. VR4 polynucleotides can also be obtained from natural sources such as genomic DNA libraries or can be synthesized using well known and commercially available techniques. EP202352.1 further discloses methods for the recombinant production of VR4 polypeptides, including expression vectors and hosts and details of purification methods.

This invention also relates to the use of polynucleotides of the present invention as diagnostic reagents useful in the detection of diseases caused by over or underexpression of VR4 polypeptide, or expression of a mutated form of VR4, in a subject. Such diseases include diseases of cartilage, such as hyaline-, fibro- and elastic-cartilage, or diseases of

tissues where such cartilage is found including diseases or disorders affecting the larynx, auditory canal, intervertebral discs, ligaments, tendons and joint capsules, bone development including osteoporosis, diseases involving joint destruction and also pain linked to rheumatoid arthritis and osteoarthritis.

- 5 Detection of a mutated form of the gene characterised by the polynucleotide of SEQ ID NO:1 which is associated with a dysfunction will provide a diagnostic tool that can add to, or define, a diagnosis of a disease, or susceptibility to a disease, which results from under-expression, over-expression or altered expression of the VR4 gene. Individuals carrying mutations in the gene may be detected at the DNA level by a variety of techniques.
- 10 Nucleic acids for diagnosis may be obtained from a subject's cells, such as from blood, urine, saliva, tissue biopsy or autopsy material. The genomic DNA may be used directly for detection or may be amplified enzymatically by using PCR or other amplification techniques prior to analysis. RNA or cDNA may also be used in similar fashion. Deletions and insertions can be detected by a change in size of the amplified
- 15 product in comparison to the normal genotype. Point mutations can be identified by hybridizing amplified DNA to labeled VR4 nucleotide sequences. Perfectly matched sequences can be distinguished from mismatched duplexes by Rnase digestion or by differences in melting temperatures. DNA sequence differences may also be detected by alterations in electrophoretic mobility of DNA fragments in gels, with or without denaturing
- 20 agents, or by direct DNA sequencing (see, e.g., Myers *et al.*, Science (1985) 230:1242). Sequence changes at specific locations may also be revealed by nuclease protection assays, such as Rnase and S1 protection or the chemical cleavage method (see Cotton *et al.*, Proc Natl Acad Sci USA (1985) 85: 4397-4401). In another embodiment, an array of oligonucleotides probes comprising VR4 nucleotide sequence or fragments thereof can be
- 25 constructed to conduct efficient screening of e.g., genetic mutations. Array technology methods are well known and have general applicability and can be used to address a variety of questions in molecular genetics including gene expression, genetic linkage, and genetic variability (see for example: M.Chee *et al.*, Science, Vol 274, pp 610-613 (1996)).

- 30 The diagnostic assays offer a process for diagnosing or determining a susceptibility to the Diseases through detection of mutation in the VR4 genes by the methods described. In addition, such diseases may be diagnosed by methods comprising determining from a sample derived from a subject an abnormally decreased or increased level of polypeptide

P32689

or mRNA. Decreased or increased expression can be measured at the RNA level using any of the methods well known in the art for the quantitation of polynucleotides, such as, for example, nucleic acid amplification, for instance PCR, RT-PCR, Rnase protection, Northern blotting and other hybridization methods. Assay techniques that can be used to determine levels of a protein, such as a polypeptide of the present invention, in a sample derived from a host are well-known to those of skill in the art. Such assay methods include radioimmunoassays, competitive-binding assays, Western Blot analysis and ELISA assays.

Thus in another aspect, the present invention relates to a diagnostic kit which comprises:

- 10 (a) a polynucleotide of the present invention, preferably the nucleotide sequence of SEQ ID NO: 1 or a fragment thereof ;
- (b) a nucleotide sequence complementary to that of (a);
- (c) a polypeptide of the present invention, preferably the polypeptide of SEQ ID NO:2 or a fragment thereof; or
- 15 (d) an antibody to a polypeptide of the present invention, preferably to the polypeptide of SEQ ID NO:2.

It will be appreciated that in any such kit, (a), (b), (c) or (d) may comprise a substantial component. Such a kit will be of use in diagnosing diseases of cartilage, such as hyaline-, fibro- and elastic-cartilage, or diseases of tissues where such cartilage is found including diseases or disorders affecting the larynx, auditory canal, intervertebral discs, ligaments, tendons and joint capsules, bone development including osteoporosis, diseases involving joint destruction and also pain linked to rheumatoid arthritis and osteoarthritis.

VR4 polypeptides or their fragments or analogs thereof, or cells expressing them, can also be used as immunogens to produce antibodies immunospecific for polypeptides of the present invention. The term "immunospecific" means that the antibodies have substantially greater affinity for the polypeptides of the invention than their affinity for other related polypeptides in the prior art.

Antibodies generated against VR4 polypeptides may be obtained by administering the polypeptides or epitope-bearing fragments, analogs or cells to an animal, preferably a non-human animal, using routine protocols. For preparation of monoclonal antibodies, any technique which provides antibodies produced by continuous cell line cultures can be used.

Examples include the hybridoma technique (Kohler, G. and Milstein, C., *Nature* (1975) 256:495-497), the trioma technique, the human B-cell hybridoma technique (Kozbor *et al.*, *Immunology Today* (1983) 4:72) and the EBV-hybridoma technique (Cole *et al.*, *Monoclonal Antibodies and Cancer Therapy*, 77-96, Alan R. Liss, Inc., 1985).

5 Techniques for the production of single chain antibodies, such as those described in U.S. Patent No. 4,946,778, can also be adapted to produce single chain antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms, including other mammals, may be used to express humanized antibodies.

 Antibodies against polypeptides of the present invention may be employed to
10 diagnose or treat diseases of cartilage, such as hyaline-, fibro- and elastic-cartilage, or diseases of tissues where such cartilage is found including diseases or disorders affecting the larynx, auditory canal, intervertebral discs, ligaments, tendons and joint capsules in addition to bone development, including osteoporosis, and diseases involving joint destruction and also pain linked to rheumatoid arthritis and osteoarthritis.

15 Another aspect of the invention relates to a method for inducing an immunological response in a mammal which comprises inoculating the mammal with a polypeptide of the present invention, adequate to produce antibody and/or T cell immune response to protect said animal from the diseases hereinbefore mentioned, amongst others. Yet another aspect of the invention relates to a method of inducing immunological
20 response in a mammal which comprises, delivering a polypeptide of the present invention *via* a vector directing expression of the polynucleotide and coding for the polypeptide *in vivo* in order to induce such an immunological response to produce antibody to protect said animal from diseases.

 A further aspect of the invention relates to an immunological/vaccine
25 formulation (composition) which, when introduced into a mammalian host, induces an immunological response in that mammal to a polypeptide of the present invention wherein the composition comprises a polypeptide or polynucleotide of the present invention. The vaccine formulation may further comprise a suitable carrier. Since a polypeptide may be broken down in the stomach, it is preferably administered
30 parenterally (for instance, subcutaneous, intramuscular, intravenous, or intradermal injection). Formulations suitable for parenteral administration include aqueous and non-aqueous sterile injection solutions which may contain anti-oxidants, buffers, bacteriostats

and solutes which render the formulation isostonic with the blood of the recipient; and aqueous and non-aqueous sterile suspensions which may include suspending agents or thickening agents. The formulations may be presented in unit-dose or multi-dose containers, for example, sealed ampoules and vials and may be stored in a freeze-dried condition requiring only the addition of the sterile liquid carrier immediately prior to use. The vaccine formulation may also include adjuvant systems for enhancing the immunogenicity of the formulation, such as oil-in water systems and other systems known in the art. The dosage will depend on the specific activity of the vaccine and can be readily determined by routine experimentation.

VR4 polypeptides can be used to devise screening methods to identify compounds which modulate the activity of said VR4 polypeptides. Such modulators include compounds which stimulate (agonists) or inhibit (antagonists) the function of the VR4 polypeptides. Accordingly, in a further aspect, the present invention provides for a method of screening compounds to identify those which stimulate or which inhibit the function of the VR4 polypeptides. In general modulators of VR4, such as agonists or antagonists, may be employed for therapeutic and prophylactic purposes for such diseases as hereinbefore mentioned. Compounds may be identified from a variety of sources, for example, cells, cell-free preparations, chemical libraries, and natural product mixtures. Such modulators so-identified may be natural or modified substrates, ligands or receptors of the VR4 polypeptides; or may be structural or functional mimetics thereof (see Coligan *et al.*, Current Protocols in Immunology 1(2):Chapter 5 (1991)).

The screening method may simply measure the binding of a candidate compound to the VR4 polypeptides, or to cells or membranes bearing the VR4 polypeptide, or a fusion protein thereof by means of a label directly or indirectly associated with the candidate compound. Alternatively, the screening method may involve competition with a labeled competitor. Further, these screening methods may test whether the candidate compound results in a signal generated by activation or inhibition of the VR4 polypeptides, using detection systems appropriate to the cells bearing the VR4 polypeptide. Inhibitors of activation are generally assayed in the presence of a VR4 agonist, and the effect on activation by the agonist by the presence of the candidate compound is observed. Constitutively active polypeptides may be employed in screening methods for inverse agonists or inhibitors, in the absence of an agonist or

inhibitor, by testing whether the candidate compound results in inhibition of activation of the VR4 polypeptide. Further, the screening methods may simply comprise the steps of mixing a candidate compound with a solution containing a VR4 polypeptide to form a mixture, measuring VR4 activity in the mixture, and comparing the VR4 activity of the mixture to a standard. Fusion proteins, such as those made from Fc portion and VR4 polypeptide, as hereinbefore described, can also be used for high-throughput screening assays to identify antagonists for the polypeptide of the present invention (see D. Bennett *et al.*, J Mol Recognition, 8:52-58 (1995); and K. Johanson *et al.*, J Biol Chem, 270(16):9459-9471 (1995)).

The polynucleotides, polypeptides and antibodies to the VR4 polypeptides may also be used to configure screening methods for detecting the effect of added compounds on the production of mRNA and polypeptide in cells. For example, an ELISA assay may be constructed for measuring secreted or cell associated levels of polypeptide using monoclonal and polyclonal antibodies by standard methods known in the art. This can be used to discover agents which may inhibit or enhance the production of polypeptide (also called antagonist or agonist, respectively) from suitably manipulated cells or tissues.

Examples of potential polypeptide antagonists include antibodies or, in some cases, oligonucleotides or proteins which are closely related to the ligands, substrates or receptors of the VR4 polypeptide, e.g., a fragment of the ligands, substrates or receptors or small molecules which bind to the VR4 polypeptides of the present invention but do not elicit a response, so that the activity of the VR4 polypeptide is prevented.

Thus, in another aspect, the present invention relates to a screening kit for identifying agonists, antagonists, ligands, receptors, substrates etc. for VR4 polypeptides; or compounds which decrease or enhance the production of such VR4 polypeptides,

which comprises:

- (a) a VR4 polypeptide;
- (b) a recombinant cell expressing a VR4 polypeptide;
- (c) a cell membrane expressing a VR4 polypeptide; or
- (d) antibody to a VR4 polypeptide;

which polypeptide is preferably that of SEQ ID NO:2.

It will be appreciated that in any such kit, (a), (b), (c) or (d) may comprise a substantial component.

It will be readily appreciated by the skilled artisan that a VR4 polypeptide may also be used in a method for the structure-based design of a compound that modulates the activity of the VR4 polypeptide, by:

- (a) determining in the first instance the three-dimensional structure of the VR4 polypeptide;
- (b) deducing the three-dimensional structure for the likely reactive or binding site(s) of a modulating compound;
- (c) synthesizing candidate modulating compounds that are predicted to bind to or react with the deduced binding or reactive site; and
- (d) testing whether the candidate compounds are indeed modulators.

It will be further appreciated that this will normally be an iterative process.

In a further aspect, the present invention provides methods of treating abnormal conditions such as, for instance diseases of cartilage, such as hyaline-, fibro- and elastic- cartilage, or diseases of tissues where such cartilage is found including diseases or disorders affecting the larynx, auditory canal, intervertebral discs, ligaments, tendons and joint capsules in addition to bone development including osteoporosis, diseases involving joint destruction and also pain linked to rheumatoid arthritis and osteoarthritis, related to either an excess of, or an under-expression of, VR4 polypeptide activity.

If the activity of the VR4 polypeptide is in excess, several approaches are available. One approach comprises administering to a subject in need thereof an inhibitor compound (antagonist) as hereinabove described, optionally in combination with a pharmaceutically acceptable carrier, in an amount effective to inhibit the function of the VR4 polypeptide, such as, for example, by blocking the binding of ligands, substrates, receptors, enzymes, etc., or by inhibiting a second signal, and thereby alleviating the abnormal condition. In another approach, soluble forms of the VR4 polypeptide still capable of binding the ligand, substrate, enzymes, receptors, etc. in competition with endogenous polypeptide may be administered. Typical examples of such competitors include fragments of the VR4 polypeptide.

In still another approach, expression of the gene encoding endogenous VR4 polypeptide can be inhibited using expression blocking techniques. Known such techniques involve the use of antisense sequences, either internally generated or

externally administered (see, for example, O'Connor, J Neurochem (1991) 56:560 in Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988)). Such antisense polynucleotides are designed to comprise the antisense sequence of a polynucleotide encoding a VR4 polypeptide, or a fragment thereof. A VR4 encoding polynucleotide can include a DNA or an RNA, for example a mRNA.

Alternatively, oligonucleotides which form triple helices ("triplexes") with the gene can be supplied (see, for example, Lee *et al.*, Nucleic Acids Res (1979) 6:3073; Cooney *et al.*, Science (1988) 241:456; Dervan *et al.*, Science (1991) 251:1360). These oligomers can be administered *per se* or the relevant oligomers can be expressed *in vivo*. Synthetic antisense or triplex oligonucleotides may comprise modified bases or modified backbones. Examples of the latter include methylphosphonate, phosphorothioate or peptide nucleic acid backbones. Such backbones are incorporated in the antisense or triplex oligonucleotide in order to provide protection from degradation by nucleases and are well known in the art. Antisense and triplex molecules synthesised with these or other modified backbones also form part of the present invention.

In addition, expression of the human VR4 polypeptide may be prevented by using ribozymes specific to the human VR4 mRNA sequence. Ribozymes are catalytically active RNAs that can be natural or synthetic (see for example Usman, N, et al., Curr. Opin. Struct. Biol (1996) 6(4), 527-33.) Synthetic ribozymes can be designed to specifically cleave the human VR4 mRNAs at selected positions thereby preventing translation of the human VR4 mRNAs into functional polypeptide. Ribozymes may be synthesised with a natural ribose phosphate backbone and natural bases, as normally found in RNA molecules. Alternatively the ribozymes may be synthesised with non-natural backbones to provide protection from ribonuclease degradation, for example, 2'-O-methyl RNA, and may contain modified bases.

For treating abnormal conditions related to an under-expression of VR4 and its activity, several approaches are also available. One approach comprises administering to a subject a therapeutically effective amount of a compound which activates a VR4 polypeptide of the present invention, i.e., an agonist as described above, in combination with a pharmaceutically acceptable carrier, to thereby alleviate the abnormal condition. Alternatively, gene therapy may be employed to effect the endogenous production of VR4

by the relevant cells in the subject. For example, a polynucleotide of the invention may be engineered for expression in a replication defective retroviral vector, as discussed above. The retroviral expression construct may then be isolated and introduced into a packaging cell transduced with a retroviral plasmid vector containing RNA encoding a polypeptide of the present invention such that the packaging cell now produces infectious viral particles containing the gene of interest. These producer cells may be administered to a subject for engineering cells *in vivo* and expression of the polypeptide *in vivo*. For an overview of gene therapy, see Chapter 20, Gene Therapy and other Molecular Genetic-based Therapeutic Approaches, (and references cited therein) in Human Molecular Genetics, T Strachan and A P Read, BIOS Scientific Publishers Ltd (1996). Another approach is to administer a therapeutic amount of a VR4 polypeptide of the present invention in combination with a suitable pharmaceutical carrier.

In a further aspect, the present invention provides for pharmaceutical compositions comprising a therapeutically effective amount of a VR4 polypeptide, such as the soluble form of a VR4 polypeptide of the present invention, agonist/antagonist peptide or small molecule compound, in combination with a pharmaceutically acceptable carrier or excipient. Such carriers include, but are not limited to, saline, buffered saline, dextrose, water, glycerol, ethanol, and combinations thereof. The invention further relates to pharmaceutical packs and kits comprising one or more containers filled with one or more of the ingredients of the aforementioned compositions of the invention. VR4 polypeptides and other compounds of the present invention may be employed alone or in conjunction with other compounds, such as therapeutic compounds.

The composition will be adapted to the route of administration, for instance by a systemic or an oral route. Preferred forms of systemic administration include injection, typically by intravenous injection. Other injection routes, such as subcutaneous, intramuscular, or intraperitoneal, can be used. Alternative means for systemic administration include transmucosal and transdermal administration using penetrants such as bile salts or fusidic acids or other detergents. In addition, if a VR4 polypeptide or other compounds of the present invention can be formulated in an enteric or an encapsulated formulation, oral administration may also be possible. Administration of these compounds may also be topical and/or localized, in the form of salves, pastes, gels, and the like.

The dosage range required depends on the choice of peptide or other compounds of the present invention, the route of administration, the nature of the formulation, the nature of the subject's condition, and the judgment of the attending practitioner. Suitable dosages, however, are in the range of 0.1-100 µg/kg of subject. Wide variations in the needed dosage, however, are to be expected in view of the variety of compounds available and the differing efficiencies of various routes of administration. For example, oral administration would be expected to require higher dosages than administration by intravenous injection. Variations in these dosage levels can be adjusted using standard empirical routines for optimization, as is well understood in the art.

Polypeptides used in treatment can also be generated endogenously in the subject, in treatment modalities often referred to as "gene therapy" as described above. Thus, for example, cells from a subject may be engineered with a polynucleotide, such as a DNA or RNA, to encode a VR4 polypeptide *ex vivo*, and for example, by the use of a retroviral plasmid vector. The cells are then introduced into the subject.

The following definitions are provided to facilitate understanding of certain terms used frequently hereinbefore.

"Antibodies" as used herein includes polyclonal and monoclonal antibodies, chimeric, single chain, and humanized antibodies, as well as Fab fragments, including the products of an Fab or other immunoglobulin expression library.

"Isolated" means altered "by the hand of man" from the natural state. If an "isolated" composition or substance occurs in nature, it has been changed or removed from its original environment, or both. For example, a polynucleotide or a polypeptide naturally present in a living animal is not "isolated," but the same polynucleotide or polypeptide separated from the coexisting materials of its natural state is "isolated", as the term is employed herein.

"Polynucleotide" generally refers to any polyribonucleotide or polydeoxribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA. "Polynucleotides" include, without limitation, single- and double-stranded DNA, DNA that is a mixture of single- and double-stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically,

double-stranded or a mixture of single- and double-stranded regions. In addition, “polynucleotide” refers to triple-stranded regions comprising RNA or DNA or both RNA and DNA. The term “polynucleotide” also includes DNAs or RNAs containing one or more modified bases and DNAs or RNAs with backbones modified for stability or for other reasons. “Modified” bases include, for example, tritylated bases and unusual bases such as inosine. A variety of modifications may be made to DNA and RNA; thus, “polynucleotide” embraces chemically, enzymatically or metabolically modified forms of polynucleotides as typically found in nature, as well as the chemical forms of DNA and RNA characteristic of viruses and cells. “Polynucleotide” also embraces relatively short polynucleotides, often referred to as oligonucleotides.

“Polypeptide” refers to any peptide or protein comprising two or more amino acids joined to each other by peptide bonds or modified peptide bonds, i.e., peptide isosteres. “Polypeptide” refers to both short chains, commonly referred to as peptides, oligopeptides or oligomers, and to longer chains, generally referred to as proteins.

Polypeptides may contain amino acids other than the 20 gene-encoded amino acids. “Polypeptides” include amino acid sequences modified either by natural processes, such as post-translational processing, or by chemical modification techniques which are well known in the art. Such modifications are well described in basic texts and in more detailed monographs, as well as in a voluminous research literature. Modifications may occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present to the same or varying degrees at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications. Polypeptides may be branched as a result of ubiquitination, and they may be cyclic, with or without branching. Cyclic, branched and branched cyclic polypeptides may result from post-translation natural processes or may be made by synthetic methods. Modifications include acetylation, acylation, ADP-ribosylation, amidation, biotinylation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphatidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cystine, formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI

anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination (see, for instance, *Proteins - Structure and Molecular Properties*, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York, 1993; Wold, F., *Post-translational Protein Modifications: Perspectives and Prospects*, pgs. 1-12 in *Post-translational Covalent Modification of Proteins*, B. C. Johnson, Ed., Academic Press, New York, 1983; Seifter *et al.*, "Analysis for protein modifications and nonprotein cofactors", *Meth Enzymol* (1990) 182:626-646 and Rattan *et al.*, "Protein Synthesis: Post-translational Modifications and Aging", *Ann NY Acad Sci* (1992) 663:48-62).

"Variant" refers to a polynucleotide or polypeptide that differs from a reference polynucleotide or polypeptide, but retains essential properties. A typical variant of a polynucleotide differs in nucleotide sequence from another, reference polynucleotide. Changes in the nucleotide sequence of the variant may or may not alter the amino acid sequence of a polypeptide encoded by the reference polynucleotide. Nucleotide changes may result in amino acid substitutions, additions, deletions, fusions and truncations in the polypeptide encoded by the reference sequence, as discussed below. A typical variant of a polypeptide differs in amino acid sequence from another, reference polypeptide. Generally, differences are limited so that the sequences of the reference polypeptide and the variant are closely similar overall and, in many regions, identical. A variant and reference polypeptide may differ in amino acid sequence by one or more substitutions, additions, deletions in any combination. A substituted or inserted amino acid residue may or may not be one encoded by the genetic code. A variant of a polynucleotide or polypeptide may be a naturally occurring such as an allelic variant, or it may be a variant that is not known to occur naturally. Non-naturally occurring variants of polynucleotides and polypeptides may be made by mutagenesis techniques or by direct synthesis.

"Identity," as known in the art, is a relationship between two or more polypeptide sequences or two or more polynucleotide sequences, as determined by comparing the sequences. In the art, "identity" also means the degree of sequence relatedness between polypeptide or polynucleotide sequences, as the case may be, as determined by the match between strings of such sequences. "Identity" and "similarity" can be readily calculated by known methods, including but not limited to those described in (*Computational*

Molecular Biology, Lesk, A.M., ed., Oxford University Press, New York, 1988;
Biocomputing: Informatics and Genome Projects, Smith, D.W., ed., Academic Press,
 New York, 1993; *Computer Analysis of Sequence Data*, Part I, Griffin, A.M., and Griffin,
 H.G., eds., Humana Press, New Jersey, 1994; *Sequence Analysis in Molecular Biology*,
 5 von Heinje, G., Academic Press, 1987; and *Sequence Analysis Primer*, Gribskov, M. and
 Devereux, J., eds., M Stockton Press, New York, 1991; and Carillo, H., and Lipman, D.,
SIAM J Applied Math., 48: 1073 (1988). Preferred methods to determine identity are
 designed to give the largest match between the sequences tested. Methods to determine
 identity and similarity are codified in publicly available computer programs. Preferred
 10 computer program methods to determine identity and similarity between two sequences
 include, but are not limited to, the GCG program package (Devereux, J., et al., *Nucleic
 Acids Research* 12(1): 387 (1984)), BLASTP, BLASTN, and FASTA (Atschul, S.F. et
 al., *J. Molec Biol.* 215: 403-410 (1990). The BLAST X program is publicly available
 from NCBI and other sources (*BLAST Manual*, Altschul, S., et al., NCBI NLM NIH
 15 Bethesda, MD 20894; Altschul, S., et al., *J. Mol. Biol.* 215: 403-410 (1990). The well
 known Smith Waterman algorithm may also be used to determine identity.

Preferred parameters for polypeptide sequence comparison include the following:

1) Algorithm: Needleman and Wunsch, *J. Mol Biol.* 48: 443-453 (1970)
 Comparison matrix: BLOSSUM62 from Hentikoff and Hentikoff, *Proc. Natl. Acad. Sci.*
 20 USA. 89:10915-10919 (1992)
 Gap Penalty: 12
 Gap Length Penalty: 4

A program useful with these parameters is publicly available as the "gap"
 program from Genetics Computer Group, Madison WI. The aforementioned parameters
 25 are the default parameters for peptide comparisons (along with no penalty for end gaps).

Preferred parameters for polynucleotide comparison include the following:

1) Algorithm: Needleman and Wunsch, *J. Mol Biol.* 48: 443-453 (1970)
 Comparison matrix: matches = +10, mismatch = 0
 Gap Penalty: 50
 30 Gap Length Penalty: 3
 Available as: The "gap" program from Genetics Computer Group, Madison WI. These
 are the default parameters for nucleic acid comparisons.

By way of example, a polynucleotide sequence of the present invention may be identical to the reference sequence of SEQ ID NO:1, that is be 100% identical, or it may include up to a certain integer number of nucleotide alterations as compared to the reference sequence. Such alterations are selected from the group consisting of at least one nucleotide deletion, substitution, including transition and transversion, or insertion, and wherein said alterations may occur at the 5' or 3' terminal positions of the reference nucleotide sequence or anywhere between those terminal positions, interspersed either individually among the nucleotides in the reference sequence or in one or more contiguous groups within the reference sequence. The number of nucleotide alterations is determined by multiplying the total number of nucleotides in SEQ ID NO:1 by the numerical percent of the respective percent identity (divided by 100) and subtracting that product from said total number of nucleotides in SEQ ID NO:1, or:

$$n_n \leq x_n - (x_n \bullet y).$$

wherein n_n is the number of nucleotide alterations, x_n is the total number of nucleotides in SEQ ID NO:1, and y is, for instance, 0.70 for 70%, 0.80 for 80%, 0.85 for 85%, 0.90 for 90%, 0.95 for 95%, etc., and wherein any non-integer product of x_n and y is rounded down to the nearest integer prior to subtracting it from x_n . Alterations of a polynucleotide sequence encoding the polypeptide of SEQ ID NO:2 may create nonsense, missense or frameshift mutations in this coding sequence and thereby alter the polypeptide encoded by the polynucleotide following such alterations.

Similarly, a polypeptide sequence of the present invention may be identical to the reference sequence of SEQ ID NO:2, that is be 100% identical, or it may include up to a certain integer number of amino acid alterations as compared to the reference sequence such that the % identity is less than 100%. Such alterations are selected from the group consisting of at least one amino acid deletion, substitution, including conservative and non-conservative substitution, or insertion, and wherein said alterations may occur at the amino- or carboxy-terminal positions of the reference polypeptide sequence or anywhere between those terminal positions, interspersed either individually among the amino acids in the reference sequence or in one or more contiguous groups within the reference sequence. The number of amino acid alterations for a given % identity is determined by multiplying the total number of amino acids in SEQ ID NO:2 by the numerical percent of

the respective percent identity (divided by 100) and then subtracting that product from said total number of amino acids in SEQ ID NO:2, or:

$$n_a \leq x_a - (x_a \bullet y),$$

wherein n_a is the number of amino acid alterations, x_a is the total number of amino acids in SEQ ID NO:2, and y is, for instance 0.70 for 70%, 0.80 for 80%, 0.85 for 85% etc., and wherein any non-integer product of x_a and y is rounded down to the nearest integer prior to subtracting it from x_a .

"Homolog" is a generic term used in the art to indicate a polynucleotide or polypeptide sequence possessing a high degree of sequence relatedness to a subject sequence. Such relatedness may be quantified by determining the degree of identity and/or similarity between the sequences being compared as hereinbefore described. Falling within this generic term are the terms "ortholog", meaning a polynucleotide or polypeptide that is the functional equivalent of a polynucleotide or polypeptide in another species, and "paralog" meaning a functionally similar sequence when considered within the same species.

"Fusion protein" refers to a protein encoded by two, often unrelated, fused genes or fragments thereof. In one example, EP-A-0 464 discloses fusion proteins comprising various portions of constant region of immunoglobulin molecules together with another human protein or part thereof. In many cases, employing an immunoglobulin Fc region as a part of a fusion protein is advantageous for use in therapy and diagnosis resulting in, for example, improved pharmacokinetic properties [see, e.g., EP-A 0232 262]. On the other hand, for some uses it would be desirable to be able to delete the Fc part after the fusion protein has been expressed, detected and purified.

Examples

Example 1 – VR4 is expressed in cartilage and chondrocytes.

- 5 Tissue and cell expression of human VR4 was studied using TaqMan (Perkin Elmer) quantitative RT-PCR (Gibson et al. (1996) Genome Res. 1996 Oct;6(10):995-1001) according to the manufacturers instructions. TaqMan reactions were conducted using probes for human GAPDH, cyclophilin and human VR4. The human VR4 probe consisted of:
- 10 5'-ATGAGGACCAGACCAACTGCA (SEQ ID NO:3) and 5'-GGAGGAAGGTGCTGAAGGTCTC (SEQ ID NO:4) flanking primers and a 5'-CACTTACCCCTCGTGCCGTGACAG (SEQ ID NO:6) fluorogenic probe. Data were analysed using the Power Macintosh software accompanying the ABI Prism™ 7700.

15

Result: The data from a screen of body tissues, shown in Table 1, shows that human VR4 is most prominently expressed in cartilage. A screen of primary and clonal cell cultures shows significant expression only in chondrocytes.

- 20 Table 1. Relative mRNA expression in human tissues and cell-lines. The figures indicate a quantitative score from 1 (low expression) to 5 (very high expression).

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T
T	0	1	0	1	1	1	2	0	0	0	1	0	0	1	1	1	2	5	1	0
C	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	0	0

T relates to the category of different body tissues as follows:

- 25 A CNS, B pituitary, C heart,
D lung, E liver, F foetal liver,
G kidney, H skeletal muscle, I stomach,
J intestine, K spleen, L lymphocytes,
M macrophages, N adipose, O pancreas,
P prostate, Q placenta, R cartilage,

S bone, T bone marrow.

C relates to the category of different cell lines as follows:

A aortic smooth muscle cells, B bladder smooth muscle cells,

- 5 C C20A4, D MG63, E SAOS2,
 F lymphocyte, G macrophage, H platelets,
 I neutrophil, J CHANG, K HepG2,
 L IMR32, M SK-N-MC, N SK-N-SH,
 O NT-2, P 1321N1, Q C13,
 10 R primary human chondrocytes, S Hs-683,
 T HEK293.

The results show high-level expression in cartilage tissue (T, R) and primary human chondrocytes (C,R).

15

Example 2 - VR4 is activated by 4 α -phorbol-12, 13 didecanoate.

The VR4 cDNA was inserted into the expression vector pcDNA3.1 V5-His (Invitrogen). Wildtype HEK293 cells, or HEK293 cells transfected with the human VR4:pcDNA3.1 V5-His construct, or mock transfected cells, or bovine chondrocytes, were seeded into
 20 96-well microtitre plates at 25,000 cells/well and cultured overnight. The cells were then incubated with 4microM Fluo-3 for 2hrs at room temperature in the dark. Dye loaded cells were washed 4x with Tyrodes buffer: (NaCl, 145mM; KCl, 2.5mM; Hepes, 10mM; Glucose, 10mM; MgCl₂, 1.2mM; CaCl₂, 1.5mM), which also contained 0.2% BSA but not probenecid. Agonists and antagonists were also prepared in Tyrodes buffer. Cells
 25 were preincubated for 30mins with antagonist or buffer. Agonist addition and measurement of cytoplasmic calcium concentration was performed in the FLIPR (Smart et al., (2000) Br. J. Pharmacol. 129, 227-230).

Results:

- 30 Both phorbol 12-myristate 13-acetate (PMA) and 4 α -phorbol-12,13-didecanoate (4 α PDD) increased intracellular calcium in HEK293-VR4 cells (Table 1) but were without effect in wild type HEK293 cells or in cells transfected with empty vector. PMA also activated

VR1, but was only a partial agonist (E_{max} 0.46) compared to capsaicin and RTX. 4 α PDD was inactive at VR1 (Table 1).

Table 1

	pEC50			
	wild type	empty vector	hVR1	hVR4
RTX	IA	IA	8.93 \pm 0.20	IA
capsaicin	IA	IA	7.48 \pm 0.12	IA
PMA	IA	IA	7.86 \pm 0.06	6.64 \pm 0.06
4 α PDD	IA	IA	IA	5.73 \pm 0.06

- 5 Data are mean \pm s.e.mean, where n=3-5. IA= inactive
 hVR1 is human VR1
 hVR4 is human VR4

In conclusion, 4 α PDD acts as a VR4 selective agonist.

10

Bovine articular chondrocytes responded to 4 α -PDD with a similar dose dependency as the transfected HEK293 cells. The response to 4 α -PDD had a similar kinetic profile and concentration dependency to that seen for the recombinant VR4 expressed in HEK293 cells. The response was dependent upon extracellular calcium ions and was blocked by

15 the channel blocker ruthenium red. These data suggest that the response to 4 α -PDD was due to the VR4 endogenously expressed by chondrocytes.

SEQUENCE INFORMATION

SEQ ID NO:1

ATGCGCGGATTCACAGCAAGAGGCCCGCGCGGGGCCGGGAGGTGGCTGAGCTCCCCGGG
 GATGAGAGTGGCACCCAGGTGGGGAGGCTTTTCCCTCTCTCCCTCCCTGGCCAAATCTGTTT
 5 GAGGGGGAGGATGGCTCCCTTTTCGCCCTCACCGGCTGATGCCAGTCCGCCCTGCTGGCCCA
 GGCGATGGGCGACCAAATCTGCGCATGAAGTTCACAGGGCGCTTCCGCAAGGGGGTGCCC
 AACCCCATCGATCTGCTGGAGTCCACCCTATATGAGTCCCTCGGIGGTGCCCTGGGCCCAAG
 AAAGCACCCATGGACTCACTGTTTGACTACGGGCACCTATCGTCAACACTCCAGTGACAAC
 AAGAGGTGGAGGAAGAAGATCATAGAGAAGCAGCCGCAGAGCCCCAAAGCCCCTGCCCC
 10 CAGCCGCCCCCATCTCTCAAAGTCTTCAACCGGCTATCTCTTTTGACATCGTGTCCCGG
 GGCTCCACTGCTGACCTGGACGGGCTGCTCCCATTTCTTGCTGACCCACAAGAAACGCCTA
 ACTGATGAGGAGTTTCGAGAGCCATCTACGGGGAAGACCTGCCGTGCCCAAGGCCCTTGCTG
 AACCTGAGCAATGGCCGCAACGACACCATCCCTGTGCTGCTGGACATCGCGGAGCGCACC
 GGCAACATGCGGGAGTTCATTAACTCGCCCTTCCGIGACATCTACTATCGAGGTGAGACA
 15 GCCCCGACATCGCCATTGAGCGTCGCTGCAAACACTACGTGGAACTTCTCGTGGCCCAG
 GGAGCTGAATGTCACGCCCAGGCCCTGTTGGGCGCTTCTTCCAGCCCAAGGATGAGGGGGG
 TACTTCTACTTTGGGGAGCTGCCCCGTGTCGCTGGCTGCCGTGCACCAACCAGCCCCACATT
 GTCAACTACCTGACGGAGAACCCCCACAAGAAGGCGGACATGCGGCGCCAGGACTCGCGA
 GGCAACACAGTGCCTGCATGCGCTGGTGGCCATTGCTGACAACACCCGTGAGAACACCAAG
 20 TTTGTTACCAAGATGTACGACCTGCTGCTGCTCAAGTGTGCCCGCCTCTTCCCCGACAGC
 AACCTGGAGGCCGTGCTCAACAACGACGGCTCTCGCCCCTCATGATGGCTGCCAAGACG
 GGCAAGATTGGGATCTTTCAGCACATCATCCGGCGGGAGGTGACGGATGAGGACACACGG
 CACCTGTCCCGCAAGTTCAAGGACTGGGCCATATGGGCCAGTGTATTCTCTCGCTTTATGAC
 CTCTCCCTCCCTGGACACGTGTGGGGAAGAGGCCCTCCGTGCTGGAGATCCTGGTGTACAAC
 25 AGCAAGATTGAGAACCGCCACGAGATGCTGGCTGTGGAGCCCATCAATGAACCTGCTGCGG
 GACAAGTGGCGCAAGTTGCGGGCCGTCTCCTTCTACATCAACGTGGTCTCCTACCTGTGT
 GCCATGGTCACTCTTCACTCTCACCGCCTACTACAGCCGCTGGAGGGCACACCGCCGTAC
 CCTTACCGCAACACGGTGGACTACCTGCGGCTGGCTGGCGAGGTCAATTACGCTCTTCACT
 GGGGTCTCTGTTCTTCTTACCAACATCAAAGACTTGTTTCAATGAAGAAATGCCCTGGAGTG
 30 AATTCTCTCTTCATTGATGGCTCCTTCCAGCTGCTCTACTTCATCTACTCTGTCTGGTG
 ATCGTCTCAGCAGCTCTTACCTGGCAGGGATCGAGGCCCTACCTGGCCGTGATGGTCTTT
 GCCCTGGTCTCTGGCTGGATGAATGCCCTTTACTTTACCCGTGGGCTGAAGCTGACGGGG
 ACTTAATAGCATCATGATCCAGAAGATTCTCTTCAAGGACCTTTTCCGATTCCTGCTCGTC
 TACTTGCTCTTTCATGATCGGCTACGCTTCAGCCCTGGTCTCCCTCTTGAACCCGTGTGCC
 35 AACATGAAGGTGTCAATGAGGACCAGACCAACTGCACAGTGCCCACTTACCCCTCGTGC
 CGTGACAGCGAGACCTTCAGCACCTTCTCCTGGACCTGTTTAAAGCTGACCATTGGCATG
 GCGGACCTGGAGATGCTGAGCAGCACCAAGTACCCCTGGTCTTCAATCATCCTGCTGGTG
 ACCTACATCATCTTACCTTTGTGCTGCTCCTCAACATGCTCATGCCCCTCATGGGCGAG
 ACAGTGGGTGAGGTCTTAAASGAGAGCAAGCACATCTGGAAGCTGCACTGGGCCACCAAC

ATCCTGGACATTGAGCGCTCCTTCCCCGTATTCTTGAGGAAGGCCCTCCGCTCTGGGGAG
 ATGGTCACCGTGGGCAAGAGCTCGGACGGCACTCCTGACCGCAGGTGGTGC'TTCAGGGTG
 GATGAGGTGAACTGGICTCACTGGAACCAGAACTTGGGCATCATCAACGAGGACCCGGGC
 AAGAATGAGACCTACCACTATTATGGCTTCTCGCATACCGTGGGCCGCC'TCCGCAGGGAT
 5 CGCTGGTCCTCGGTGGTACCCCGCTGGTGGAAGTGAACAAGAACTCGAACCCGGACGAG
 GTGGTGGTGCCTCTGGACAGCATGGGGAACCCCGCTGCGATGGCCACCAGCAGGGTTAC
 CCCCACAAGTGGAGGACTGATGACGCCCCGCTCTAG

SEQ ID NO:2

10 MADSSSEGPRAGPGEVAELPGDESGTPGGEAFPLSSLANLFEGEDGSLSPSPADASRPAGF
 GDGRPNLRMKFQGAFRKGVNPNIDLLESTLYESSVVPKPKAPMDSLFDYGTyrHHSSDN
 KRWRKKZIEKQPQSPKAPAPQPPFILKVENRPILEFDIVSRGSTADLDGLLPFLLTHKKRL
 TDEEFREPSTGKTCPLKALLNLSNGRNDTIFVLLDIAERTGNMREFINSFPRDIYYRGQT
 ALHIAIERCKHYVELLVAQGADVHAQARGRFFQPKDEGGYFYFGELPLSLAAC'TNQPHI
 15 VNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFVTKMYDLLLLKCARLFPDS
 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD
 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLEC
 AMVIFTLTAYYQPLEGTPPYPYRTTVDYLRAGEVITLFTGVLEFFFTNIKDLFMKKCPGV
 NSLFIDGSFQLLYFIYSVLVIVSAALYLAGIEAYLAVMVFALVLGWMNALYFTRGLKLTG
 20 TYSIMIQKILFKDLERFLLVYLLEMIGYASALVSLNPCANMKVCNEDQTNCTVPTYPS
 RDSETFSTFLLDLEKLTIGMGDLEMLSSTKYPVVFIIILLVTYIIILTFVLLLNMLIALMGE
 TVGQVSKEKHIWKLQWATTILDIERSFVFLRKAFRSGEMVTVGKSSDGTTPDRRWCFRV
 DEVNWSHWNQNLGIINEDPGKNETYQYYGFSHTVGRLLRRDRWSSVVPVVELNKNNSNPDE
 VVVFELDSMGNPRCDGHQQGYPRKWRTDDAPL

Claims

1. The use of a compound selected from:
 - 5 (a) a VR4 polypeptide;
 - (b) a compound which modulates the activity of a VR4 polypeptide;
 - (c) a polynucleotide encoding a VR4 polypeptide; or
 - (d) an antisense polynucleotide to a polynucleotide encoding a VR4 polypeptide,for the manufacture of a medicament for treating diseases of cartilage and/or bone, or for
10 the treatment of pain associated therewith.
2. The use according to claim 1 wherein the disease is one affecting the larynx, auditory canal, intervertebral discs, ligaments, tendons and joint capsules; or a disease associated with bone development including osteoporosis; or diseases involving joint
15 destruction.
3. The use according to claim 2 wherein the diseases involving joint destruction is rheumatoid arthritis or osteoarthritis.
- 20 4. The use according to claim 1 wherein the pain is associated with rheumatoid arthritis or osteoarthritis.
5. The use according to any one of claims 1 to 4 wherein the compound which modulates the activity of a VR4 polypeptide is an agonist.
25
6. The use according to any one of claims 1 to 4 wherein the compound which modulates the activity of a VR4 polypeptide is an antagonist.
7. The use according to any one of claims 1 to 4 wherein the compound is a VR4
30 polypeptide which comprises a polypeptide having at least 95% identity to the VR4 polypeptide of SEQ ID NO:2.

8. The use according to claim 7 wherein the compound is the VR4 polypeptide of SEQ ID NO:2.
9. The use according to any one of claims 1 to 4 wherein the compound comprises
5 a polynucleotide encoding a polypeptide having at least 95% identity with the amino acid sequence of SEQ ID NO:2.
10. The use according to claim 9 wherein the polynucleotide comprises a polynucleotide having at least 95% identity with the polynucleotide of SEQ ID NO:1.
10
11. The use according to any one of claims 9 or 10 wherein the polynucleotide has the polynucleotide sequence of SEQ ID NO:1.
12. A method for screening to identify compounds that stimulate or inhibit the
15 function or level of the polypeptide as defined in claim 7 comprising a method selected from the group consisting of:
- (a) measuring or, detecting, quantitatively or qualitatively, the binding of a candidate compound to the polypeptide or a fusion protein thereof by means of a label directly or indirectly associated with the candidate compound;
- 20 (b) measuring the competition of binding of a candidate compound to the polypeptide or a fusion protein thereof in the presence of a labeled competitor;
- (c) testing whether the candidate compound results in a signal generated by activation or inhibition of the polypeptide, using detection systems appropriate to the polypeptide; or
- 25 (d) mixing a candidate compound with a solution containing a polypeptide of claim 2 or 4, to form a mixture, measuring activity of the polypeptide in the mixture, and comparing the activity of the mixture to a control mixture which contains no candidate compound.

SEQUENCE LISTING

5 <110> SmithKline Beecham plc

 <120> New Use

10 <130> P32689

 <160> 5

 <170> FastSEQ for Windows Version 3.0

15 <210> 1

 <211> 2616

 <212> DNA

 <213> Homo sapiens

20 <400> 1

atggcggatt ccagcgaagg cccccgcgcg gggcccgggg aggtggctga gctccccggg 60

gatgagagty gcacccacag tggggagggc ttccctctct cctccctggc caatctgttt 120

gagggggagtg atggctccct ttgcacctca ccggctgatg ccagtcgccc tgcctggccca 180

25 ggcgatgggc gaccaaactc gcgcataaag ttccaggggc ccttccgcaa ggggggtgcc 240

aaccccatcg atctgcttga gtccacccta tatgagtcct cgggtgggtgc tgggcccacg 300

aaagcaccga tggactcact gtttgactac ggcacctatc gtcaccactc cagtgcacaac 360

aagaggttga ggaagaagat catagagaag cagccgcaga gccccaaagc ccctgcccct 420

cagccgcccc ccactcctca agtcttcaac cggcctatcc tctttgacat cgtgtcccg 480

30 ggctccactg ctgacctgga cgggctgttc ccattcttgc tgaccacaa gaaacyccta 540

actgatgagg agtttcgaga gccatctacg ggggaagacct gcctgcccac ggcccttgcctg 600

aacctgagca atggccgcaa cgcaccatc cctgtgtctg tggacatcgc ggagcgcacc 660

ggcaacatgc gggagtccat taactcgccc ttccgtgaca tctactatcg aggtcagaca 720

gccttgcaca tcgccattga gcgtcgctgc aaacactacg tggaaacttc cgtggcccag 780

35 ggagctgatg tccacgccc ggcctgtggg cgttctcttc agcccaggga tgaggggggc 840

tactttactc ttgggggctt gccctgtcgc ctggctgcct gcaccaacca gcccacatt 900

gtcaactacc taccggagaa cccccacaag aaggcggaca tgcggcgcca ggactcgcga 960

ggcaacacag tgcacatgc gctggtgacc attgctgaca aacccgtga gaacaccaag 1020

tttgttacca agatgtacga cctgctgctg ctcaagtgtg ccgacctctt ccccgacagc 1080

40 aacctggagg ccgttctcaa caacgacggc ctctcgcccc tcatgatgac tgccaagacg 1140

ggcaagattg gcatcttca gcacatcacc cggcgggagc tgcagatga ggcacacgg 1200

cacctgtccr gcaatttcaa ggaatgggac tatgggccag tctattcttc gctttatgac 1260

ctctctctcc tgcacatg tggggaagag gcttcgtatc tggagatcct ggtatataac 1320

agcaagattg agaaccqcca cgagatgctg gctgtggagc ccatcaatga actgctgcgg 1380
 gacaagtggc gcaagttcgg ggccgtctcc ttctacatca acgtgggtctc ctacctgtgt 1440
 gccatggtca tcttcaactct caccgcctac taccagccgc tggagggcac accgccgtac 1500
 ccttaccgca ccacggtgga ctacctgcgg ctggctggcg aggtcattac gctcttcaact 1560
 5 ggggtcctgt tcttcttcac caacatcaaa gacttggtca tgaagaaatg ccttgagatg 1620
 aattctctct tcattgatgg ctccctccag ctgctctact tcacttactc tgtcctgggtg 1680
 atcgtctcag cagccctcta cctggcaggg atcgaggcct acctggccgt gatggctctt 1740
 gccctgggtc tgggctggat gaatgccctt tacttcaccc gtgggctgaa gctgacgggg 1800
 acctatagca tcatgatcca gaagattctc ttcaaggacc ttttccgatt cctgctcgtc 1860
 10 tacttgcctc tcatgatcgg ctacgcttca gccctgggtc cctcctgaa cccgtgtgcc 1920
 aacatgaagg tgtgcaatga ggaccagacc aactgcacag tgcccaacta cccctcgtgc 1980
 cgtgacagcg agaccttcag caccctctc ctggacctgt ttaagctgac cattggcatg 2040
 ggcgacctgg agatgctgag cagcaccaag taccocgtgg tcttcatcat cctgctgggtg 2100
 acctacatca tcttcacctt tgtgctgctc ctcaacatgc tcattgccct catgggcgag 2160
 15 acagtggggc aggtctccaa ggagagcaag cacatctgga agctgcagtg ggccaccacc 2220
 atcctggaca ttgagcgtc cttecccgta ttcttgagga aggccttccg ctctggggag 2280
 atggtcaccg tgggcaagag ctcggaacgg actcctgacc gcaggtggtg cttcaggggtg 2340
 gatgaggtga actggtctca ctggaaccag aacttgggca tcatcaacga ggaccggggc 2400
 aagaatgaga cctaccagta ttatggcttc tcgcataccg tgggccgcct ccgcagggat 2460
 20 cgtggtcct cgttgggtacc ccgcgtgggtg gaactgaaca agaactcgaa cccggacgag 2520
 gtggtgggtc ctctggacag catggggaac cccgcgtgcg atggccacca gcagggttac 2580
 cccgcgaagt ggaggaactga tgacgccccg ctctag 2616

<210> 2

25

<211> 871

<212> FRT

<213> Homo sapiens

<400> 2

30

Met Ala Asp Ser Ser Glu Gly Pro Arg Ala Gly Pro Gly Glu Val Ala

1

5

10

15

Glu Leu Pro Gly Asp Glu Ser Gly Thr Pro Gly Gly Glu Ala Phe Pro

20

25

30

Leu Ser Ser Leu Ala Asn Leu Phe Glu Gly Glu Asp Gly Ser Leu Ser

35

35

40

45

Pro Ser Pro Ala Asp Ala Ser Arg Pro Ala Gly Pro Gly Asp Gly Arg

50

55

60

Pro Asn Leu Arg Met Lys Phe Gln Gly Ala Phe Arg Lys Gly Val Pro

65

70

75

80

40

Asn Pro Ile Asp Leu Leu Glu Ser Thr Leu Tyr Glu Ser Ser Val Val

85

90

95

Pro Gly Pro Lys Lys Ala Pro Met Asp Ser Leu Phe Asp Tyr Gly Thr

100

105

110

Tyr Arg His His Ser Ser Asp Asn Lys Arg Trp Arg Lys Lys Ile Ile
 115 120 125
 Glu Lys Gln Pro Gln Ser Pro Lys Ala Pro Ala Pro Gln Pro Pro Pro
 130 135 140
 5 Ile Leu Lys Val Phe Asn Arg Pro Ile Leu Phe Asp Ile Val Ser Arg
 145 150 155 160
 Gly Ser Thr Ala Asp Leu Asp Gly Leu Leu Pro Phe Leu Leu Thr His
 165 170 175
 10 Lys Lys Arg Leu Thr Asp Glu Glu Phe Arg Glu Pro Ser Thr Gly Lys
 180 185 190
 Thr Cys Leu Pro Lys Ala Leu Leu Asn Leu Ser Asn Gly Arg Asn Asp
 195 200 205
 Thr Ile Pro Val Leu Leu Asp Ile Ala Glu Arg Thr Gly Asn Met Arg
 210 215 220
 15 Glu Phe Ile Asn Ser Pro Phe Arg Asp Ile Tyr Tyr Arg Gly Gln Thr
 225 230 235 240
 Ala Leu His Ile Ala Ile Glu Arg Arg Cys Lys His Tyr Val Glu Leu
 245 250 255
 20 Leu Val Ala Gln Gly Ala Asp Val His Ala Gln Ala Arg Gly Arg Phe
 260 265 270
 Phe Gln Pro Lys Asp Glu Gly Gly Tyr Phe Tyr Phe Gly Glu Leu Pro
 275 280 285
 Leu Ser Leu Ala Ala Cys Thr Asn Gln Pro His Ile Val Asn Tyr Leu
 290 295 300
 25 Thr Glu Asn Pro His Lys Lys Ala Asp Met Arg Arg Gln Asp Ser Arg
 305 310 315 320
 Gly Asn Thr Val Leu His Ala Leu Val Ala Ile Ala Asp Asn Thr Arg
 325 330 335
 30 Glu Asn Thr Lys Phe Val Thr Lys Met Tyr Asp Leu Leu Leu Leu Lys
 340 345 350
 Cys Ala Arg Leu Phe Pro Asp Ser Asn Leu Glu Ala Val Leu Asn Asn
 355 360 365
 Asp Gly Leu Ser Pro Leu Met Met Ala Ala Lys Thr Gly Lys Ile Gly
 370 375 380
 35 Ile Phe Gln His Ile Ile Arg Arg Glu Val Thr Asp Glu Asp Thr Arg
 385 390 395 400
 His Leu Ser Arg Lys Phe Lys Asp Trp Ala Tyr Gly Pro Val Tyr Ser
 405 410 415
 Ser Leu Tyr Asp Leu Ser Ser Leu Asp Thr Cys Gly Glu Glu Ala Ser
 420 425 430
 40 Val Leu Glu Ile Leu Val Tyr Asn Ser Lys Ile Glu Asn Arg His Glu
 435 440 445
 Met Leu Ala Val Glu Pro Ile Asn Glu Leu Leu Arg Asp Lys Trp Arg

	450		455		460	
	Lys Phe Gly Ala Val	Ser Phe Tyr Ile Asn Val	Val Ser Tyr Leu Cys			
	465	470	475	180		
5	Ala Met Val Ile Phe Thr Leu Thr Ala Tyr Tyr Gln Pro Leu Glu Gly					
		485	490	495		
	Thr Pro Pro Tyr Pro Tyr Arg Thr Thr Val Asp Tyr Leu Arg Leu Ala					
		500	505	510		
	Gly Glu Val Ile Thr Leu Phe Thr Gly Val Leu Phe Phe Thr Asn					
		515	520	525		
10	Ile Lys Asp Leu Phe Met Lys Lys Cys Pro Gly Val Asn Ser Leu Phe					
		530	535	540		
	Ile Asp Gly Ser Phe Gln Leu Leu Tyr Phe Ile Tyr Ser Val Leu Val					
		545	550	555	560	
	Ile Val Ser Ala Ala Leu Tyr Leu Ala Gly Ile Glu Ala Tyr Leu Ala					
15		565	570	575		
	Val Met Val Phe Ala Leu Val Leu Gly Trp Met Asn Ala Leu Tyr Phe					
		580	585	590		
	Thr Arg Gly Leu Lys Leu Thr Gly Thr Tyr Ser Ile Met Ile Gln Lys					
		595	600	605		
20	Ile Leu Phe Lys Asp Leu Phe Arg Phe Leu Leu Val Tyr Leu Leu Phe					
		610	615	620		
	Met Ile Gly Tyr Ala Ser Ala Leu Val Ser Leu Leu Asn Pro Cys Ala					
		625	630	635	640	
	Asn Met Lys Val Cys Asn Glu Asp Gln Inr Asn Cys Thr Val Pro Thr					
25		645	650	655		
	Tyr Pro Ser Cys Arg Asp Ser Glu Thr Phe Ser Thr Phe Leu Leu Asp					
		660	665	670		
	Leu Phe Lys Leu Thr Ile Gly Met Gly Asp Leu Glu Met Leu Ser Ser					
		675	680	685		
30	Thr Lys Tyr Pro Val Val Phe Ile Ile Leu Leu Val Thr Tyr Ile Ile					
		690	695	700		
	Leu Thr Phe Val Leu Leu Leu Asn Met Leu Ile Ala Leu Met Gly Glu					
		705	710	715	720	
	Thr Val Gly Gln Val Ser Lys Glu Ser Lys His Ile Trp Lys Leu Gln					
35		725	730	735		
	Trp Ala Thr Thr Ile Leu Asp Ile Glu Arg Ser Phe Pro Val Phe Leu					
		740	745	750		
	Arg Lys Ala Phe Arg Ser Gly Glu Met Val Thr Val Gly Lys Ser Ser					
		755	760	765		
40	Asp Gly Thr Pro Asp Arg Arg Trp Cys Phe Arg Val Asp Glu Val Asn					
		770	775	780		
	Trp Ser His Trp Asn Gln Asn Leu Gly Ile Ile Asn Glu Asp Pro Gly					
		785	790	795	800	

Lys Asn Glu Thr Tyr Gln Tyr Tyr Gly Phe Ser His Thr Val Gly Arg
 805 810 815
 Leu Arg Arg Asp Arg Trp Ser Ser Val Val Pro Arg Val Val Glu Leu
 820 825 830
 5 Asn Lys Asn Ser Asn Pro Asp Glu Val Val Val Pro Leu Asp Ser Met
 835 840 845
 Gly Asn Pro Arg Cys Asp Gly His Gln Gln Gly Tyr Pro Arg Lys Trp
 850 855 860
 Arg Thr Asp Asp Ala Pro Leu
 10 865 870

<210> 3
 <211> 21
 <212> DNA
 15 <213> Artificial Sequence

<220>
 <223> PCR primer

20 <400> 3
 atgaggacca gaccaactgc a 21

<210> 4
 <211> 22
 25 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

30 <400> 4
 ggaggaagyt gctgaaggtc tc 22

<210> 5
 35 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 40 <223> PCR primer' probe

<400> 5
 caattacccc tctgtccctg aaag 24